

## **RAW SEQUENCE LISTING**

**Loaded by SCORE, no errors detected.**

Application Serial Number: 10609296

Source: OIPE

Date Processed by SCORE: 9/16/2008

# ***ENTERED***

<110> APPLICANT: RASMUSSEN, Poul Baad  
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 Maxygen ApS  
 Maxygen Holdings Ltd.  
 <120> TITLE OF INVENTION: NEW INTERFERON BETA-LIKE MOLECULES  
 <130> FILE REFERENCE: 0228us410  
  
 <140> CURRENT APPLICATION NUMBER:10609296  
 <141> CURRENT FILING DATE:2003-06-27  
 <150> PRIOR APPLICATION NUMBER: US/10/084,706  
 <151> PRIOR FILING DATE: 2002-02-26  
 <150> PRIOR APPLICATION NUMBER: US 60/272,116  
 <151> PRIOR FILING DATE: 2001-02-27  
 <150> PRIOR APPLICATION NUMBER: US 60/343,436  
 <151> PRIOR FILING DATE: 2001-12-21  
 <150> PRIOR APPLICATION NUMBER: US 60/302,140  
 <151> PRIOR FILING DATE: 2001-06-29  
 <150> PRIOR APPLICATION NUMBER: US 60/316,170  
 <151> PRIOR FILING DATE: 2001-08-30  
 <150> PRIOR APPLICATION NUMBER: not yet assigned  
 <151> PRIOR FILING DATE: 2002-02-19  
 <150> PRIOR APPLICATION NUMBER: DK PA 2001 00333  
 <151> PRIOR FILING DATE: 2001-03-01  
 <150> PRIOR APPLICATION NUMBER: US 09/648,569  
 <151> PRIOR FILING DATE: 2000-08-25  
 <160> NUMBER OF SEQ ID NOS: 57  
 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
  
 <210> SEQ ID NO 1  
 <211> LENGTH: 840  
 <212> TYPE: DNA  
 <213> ORGANISM: Homo sapiens  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (76)...(636)  
 <400> SEQUENCE: 1  
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 gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg  
 111  
 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu  
 1 5 10  
 ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga  
 159  
 Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly  
 15 20 25  
 ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa  
 207  
 Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln  
 30 35 40  
 ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac  
 255  
 Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp  
 45 50 55 60  
 atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc  
 303

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      Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
      65      70      75
351  gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga
      Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
      80      85      90
399  caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc
      Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
      95      100      105
447  ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa
      Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu
      110      115      120
495  gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt
      Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
      125      130      135      140
543  ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc
      Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
      145      150      155
591  aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta
      Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
      160      165      170
636  agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac
      Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
      175      180      185
696  tgaagatctc ctagcctgtg cctctgggac tggacaattg cttcaagcat tcttcaacca
      gcagatgctg tttaagtgac tgatggctaa tgtactgcat atgaaaggac actagaagat
756  tttgaaattt ttattaaatt atgagttatt tttatttatt taaattttat tttggaaaat
816  aaattatttt tgggtgcaaaa gtca
840

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<210> SEQ ID NO 2

<211> LENGTH: 166

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CHAIN

<222> LOCATION: (1)...(166)

<223> OTHER INFORMATION: hIFNB mature sequence

<400> SEQUENCE: 2

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 1      5      10      15
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
 20      25      30
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35      40      45
Gln Phe Gln Lys Glu Asp Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50      55      60
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65      70      75      80
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85      90      95
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr

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<210> SEQ ID NO 3
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 3
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70

<210> SEQ ID NO 4
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 4
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<210> SEQ ID NO 5
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 5
    gaacttcgac atccccgagg aaatcaagca gctgcagcag ttccagaagg aggacgccgc
60      tctgaccatc
70

<210> SEQ ID NO 6
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 6
    ttccgccagg actccagctc caccggttgg aacgagacca tcgtggagaa cctgctggcc
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<210> SEQ ID NO 7
<211> LENGTH: 70
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 7  
aggagaagct ggagaaggag gacttcaccc gcggaagct gatgagctcc ctgcacctga  
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agcgctacta  
70

<210> SEQ ID NO 8  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 8  
ggagtacagc cactgcgctt ggaccatcgt acgctgtggag atcctgcgca acttctactt  
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catcaaccgc  
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<210> SEQ ID NO 9  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 9  
caccacactg gactagtgga tccttatcag ttgcgcaggt agccggtcag gcggttgatg  
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aagtagaagt  
70

<210> SEQ ID NO 10  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 10  
aggcgagctg gctgtactcc ttggccttca ggtagtgcag gatgcggcca tagtagcgct  
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tcaggtgcag  
70

<210> SEQ ID NO 11  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 11  
ctccttctcc agcttctcct ccagcacggt cttcaggtgg ttgatctggt ggtacacggt  
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ggccagcagg  
70

<210> SEQ ID NO 12  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 12  
gagctggagt cctggcgga gatggcgaag atgttctgca gcatctcgta gatggtcaga  
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gcggcgctcct  
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<210> SEQ ID NO 13  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 13  
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gccacaggag  
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<210> SEQ ID NO 14  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 14  
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ggcgatctgg  
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<210> SEQ ID NO 15  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 15  
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60  
caccagcatc  
70

<210> SEQ ID NO 16  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: primer  
<400> SEQUENCE: 16  
cactgcttac tggcttatcg aaattaatac gactcactat agggagaccc aagctggcta  
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gcgtttaaac  
70

<210> SEQ ID NO 17  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE: